IN THE SPECIFICATION:

Please amend paragraph [00153] as follows:

[00153] The results demonstrated that the longer the acyl chain lengths and the lower the unsaturation index, the lower the sensitivity of TG molecular species in positive-ion ESI/S (~~Fig. 2~~Figs. 2A and 2B and Table 1) with only one recognized exception (i.e., T20:4 TG). The results demonstrated that there were no differences of sensitivity correction factors between TG regioisomers (Table 1). A least-square regressive nonlinear curve fitting was performed to obtain correction factors for sensitivity of TG molecular species (except for T20:4 TG) as follows:

$$y = 4.4979 + 0.3441p - 0.1269q - 4.845$$

$$\text{x}10^{-3}p^{*}q + 9.9\text{x}10^{-4}q^{2}, \qquad [3]$$

where y is a correction factor for sensitivity effect relative to T17:1, q is the total carbon number in the three acyl chains of a TG species, and p is the double bond number in a TG species.

Please amend paragraph [00155] as follows:

[00155] Our aforedescribed ESI/MS/MS of TG molecular species demonstrates that a set of abundant product ions could be generated by collisional activation which corresponded to the neutral loss of each fatty acid molecular species in the selected TG peak (insets in ~~Fig. 3~~Figs. 3A and 3B). Accordingly, we examined the abundance of product ions generated from TG molecular species and determined that the total number of ion counts corresponding to each fatty acid was proportional to the number of acyl chains in the parent TG molecular species (within 10% of the experimental error). For example, product ions at *m/z* 632, 606, and 584 in Fig. 3A correspond to the neutral loss of palmitic acid, oleic acid, and arachidonic acid from the lithiated 16:0/18:1/20:4 TG quasimolecular ion (*m/z* 888) which are present in a ratio of 1:1:1 (Fig. 3A). Similarly, product ions *m/z* 632 and 610 (Fig. 3B) correspond to the neutral loss of oleic acid and arachidonic acid from the lithiated 18:1/20:4/18:1 TG molecular ion (*m/z* 914) which are present in a ratio of 2:1 reflecting their abundance in the parent TG.

Therefore, we explored the possibility that positive-ion ESI tandem mass spectrometry in the neutral loss mode can provide an informative fingerprint of the TG molecular species directly from biological samples without the need for prior chromatographic separation.